# STIC Search Report
## Biotech-Chem Library

STIC Database Tracking Number: 150043


**TO: Nita M Minnifield**
**Location: rem/3c01/3c18**
**Art Unit: 1645**
**Friday, April 08, 2005**

**Case Serial Number: 10/613749**

**From: Deirdre Arnold**
**Location: Biotech-Chem Library**
**REM 1A64**
**Phone: 571-272-2532**

**Deirdre.Arnold@uspto.gov**


## Search Notes

# RUSH

*Please feel free to contact me if you have any questions or would like to amend the search.*

Thank you for using STIC services.

Regards,
Deirdre Arnold

**STIC-Biotech/ChemLib** 150043 mgj

**From:** Chan, Christina
**Sent:** Wednesday, April 06, 2005 12:02 PM
**To:** Minnifield, Nita; STIC-Biotech/ChemLib
**Subject:** RE: sequence search request

Please rush. Thanks!! Chris

*Chris Chan*
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89



-----Original Message-----
**From:** Minnifield, Nita
**Sent:** Tuesday, April 05, 2005 1:50 PM
**To:** Chan, Christina
**Subject:** sequence search request

Christina, please approve, 2 month amdt.

STIC

10/613749

Please do an commercial and interference sequence search on SEQ ID NO: 1 of the above application.

Please provide a paper copy of the results.

Thanks,
Minnifield
71976
Art Unit 1645

**********
STAFF USE ONLY

Searcher: Arnold
Searcher Phone: 2-2537
Date Searcher Picked up: 4/6/05
Date Completed: 4/8/05
Searcher Prep/Rev. Time:___
Online Time:_____

**********
Type of Search

NA#: 1 AA#:_____
Interference:____ SPDI:___
S/L:_____ Oligomer:____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

**********
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 01:02:49 ; Search time 1738 Seconds
(without alignments)
525.629 Million cell updates/sec

Title: US-10-613-749-1
Perfect score: 24
Sequence: 1 tcgtcgtttcgtcgtttcgtcgtt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 22.4 | 93.3 | 330 | 7 | CO902262 | CO902262 Mdfrt3057 |
| | 2 | 22.4 | 93.3 | 472 | 7 | CN492399 | CN492399 Mdfw20131 |
| | 3 | 22.4 | 93.3 | 550 | 7 | CO752082 | CO752082 Mdfrt3053 |
| | 4 | 22.4 | 93.3 | 603 | 7 | CN489009 | CN489009 Mdfw2018k |
| c | 5 | 21.4 | 89.2 | 463 | 4 | BG789245 | BG789245 SEAUMC009 |
| c | 6 | 21.4 | 89.2 | 663 | 8 | BZ043048 | BZ043048 lki56g02. |
| | 7 | 20.8 | 86.7 | 292 | 7 | CN497106 | CN497106 Mdfw2023n |
| c | 8 | 20.8 | 86.7 | 676 | 8 | AZ567762 | AZ567762 238PvG10 |
| c | 9 | 20.4 | 85.0 | 669 | 4 | BI736003 | BI736003 603359133 |
| | 10 | 19.8 | 82.5 | 378 | 4 | BM577231 | BM577231 170006871 |
| | 11 | 19.8 | 82.5 | 546 | 5 | BX602071 | BX602071 BX602071 |
| | 12 | 19.8 | 82.5 | 583 | 5 | BX624220 | BX624220 BX624220 |
| | 13 | 19.8 | 82.5 | 625 | 7 | CR535039 | CR535039 CR535039 |
| | 14 | 19.8 | 82.5 | 698 | 4 | BM606721 | BM606721 170006870 |
| | 15 | 19.8 | 82.5 | 779 | 5 | BX612812 | BX612812 BX612812 |
| c | 16 | 19.8 | 82.5 | 832 | 8 | CC132027 | CC132027 NDL.23F6. |
| | 17 | 19.8 | 82.5 | 850 | 8 | AZ183817 | AZ183817 SP_1002_A |
| c | 18 | 19.8 | 82.5 | 1723 | 4 | BG336153 | BG336153 602404941 |
| c | 19 | 19.8 | 82.5 | 2008 | 2 | BF205615 | BF205615 601868581 |
| c | 20 | 19.4 | 80.8 | 1025 | 4 | BG114907 | BG114907 602315114 |
| c | 21 | 19.2 | 80.0 | 523 | 4 | BG789225 | BG789225 SEAUMC009 |
| | 22 | 19.2 | 80.0 | 648 | 2 | BF296480 | BF296480 037PbF08 |
| | 23 | 19.2 | 80.0 | 652 | 2 | BF297638 | BF297638 054PbC07 |
| c | 24 | 19.2 | 80.0 | 655 | 8 | AZ571727 | AZ571727 298PvA11 |
| c | 25 | 19.2 | 80.0 | 795 | 2 | BF676744 | BF676744 602086393 |
| | 26 | 19.2 | 80.0 | 798 | 9 | CG431698 | CG431698 Bg182-T7 |
| | 27 | 19.2 | 80.0 | 995 | 9 | CNS0202Z | AL175076 Tetraodon |
| c | 28 | 19.2 | 80.0 | 1070 | 4 | BG787012 | BG787012 SEAUMC006 |
| c | 29 | 19 | 79.2 | 566 | 8 | BH386777 | BH386777 AG-ND-144 |
| | 30 | 18.8 | 78.3 | 263 | 5 | BQ790031 | BQ790031 1040-09_2 |
| | 31 | 18.8 | 78.3 | 516 | 4 | BI531385 | BI531385 1024113D0 |
| c | 32 | 18.8 | 78.3 | 564 | 4 | BJ769036 | BJ769036 BJ769036 |
| c | 33 | 18.8 | 78.3 | 699 | 9 | CL918492 | CL918492 OA_ABa002 |
| c | 34 | 18.8 | 78.3 | 821 | 4 | BG789229 | BG789229 SEAUMC009 |
| c | 35 | 18.8 | 78.3 | 1831 | 4 | BG853946 | BG853946 1024038E1 |
| | 36 | 18.8 | 78.3 | 1904 | 4 | BG844574 | BG844574 1024006H1 |
| | 37 | 18.4 | 76.7 | 125 | 7 | CK925009 | CK925009 p3fmgc_01 |
| | 38 | 18.4 | 76.7 | 330 | 5 | BU068909 | BU068909 2569_F03_ |
| | 39 | 18.4 | 76.7 | 350 | 5 | BU067629 | BU067629 1627_C02_ |
| | 40 | 18.4 | 76.7 | 383 | 5 | BU067780 | BU067780 1629_B03_ |
| | 41 | 18.4 | 76.7 | 389 | 5 | BU067830 | BU067830 1629_G02_ |
| | 42 | 18.4 | 76.7 | 1020 | 6 | CD458971 | CD458971 Fg08_01h1 |
| | 43 | 18.4 | 76.7 | 1029 | 9 | CNS02INL | AL199146 Tetraodon |
| c | 44 | 18.2 | 75.8 | 403 | 5 | BY263743 | BY263743 BY263743 |
| c | 45 | 18.2 | 75.8 | 405 | 9 | BX946038 | BX946038 Arabidops |

ALIGNMENTS

RESULT 1
CO902262
LOCUS CO902262 330 bp mRNA linear EST 16-AUG-2004
DEFINITION Mdfrt3057k02.y1 Mdfrt Malus x domestica cDNA clone Mdfrt3057k02 5', mRNA sequence.
ACCESSION CO902262
VERSION CO902262.1 GI:51292565
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 330)
AUTHORS Korban,S., Vodkin,L., Liu,L., Gasic,K., Gonzales,O., Hernandez,A., Aldwinckle,H., Malnoy,M., Carroll,N., Goldsbrough,P., Orvis,K., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I., Tsagareishvili,R., Kennedy,S., Waterston,R. and Wilson,R.
TITLE Apple Functional Genomics grant - NSF 0321702
JOURNAL Unpublished (2004)
COMMENT Contact: Schuyler S. Korban
Apple Functional Genomics grant - NSF 0321702
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library materials provided by: Schuyler S. Korban Library constructed by: K. Gasic Library sequenced by: Washington University Genome Sequencing Center
WashU EST name: aaj94f01.y1
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers
source 1. .330
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="Mdfrt3057k02"
/lab_host="DH10B ampicillin resistant"
/clone_lib="Mdfrt"
/note="Vector: pBluescript II SK (+); Site_1: NotI; Site_2: EcoR1I; Total RNA was extracted separately from each stage [young fruitlet(<1cm), young fruitlet (1 cm dia.), young fruitlet (12cm dia.), maturing fruit I, maturing fruit II, mature fruit], using the 'pine tree' method. Poly(A)+mRNA was isolated twice from total RNA

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 01:53:14 ; Search time 284 Seconds
(without alignments)
512.113 Million cell updates/sec

Title: US-10-613-749-1
Perfect score: 24
Sequence: 1 tcgtcgtttcgtcgtttcgtcgtt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 24 | 100.0 | 24 | 17 | US-10-613-749-1 | Sequence 1, Appli |
| | 2 | 24 | 100.0 | 24 | 18 | US-10-816-220-148 | Sequence 148, App |
| | 3 | 24 | 100.0 | 24 | 18 | US-10-816-220-224 | Sequence 224, App |
| | 4 | 24 | 100.0 | 24 | 19 | US-10-644-052A-36 | Sequence 36, Appl |
| | 5 | 24 | 100.0 | 24 | 19 | US-10-644-052A-270 | Sequence 270, App |
| | 6 | 24 | 100.0 | 24 | 19 | US-10-644-052A-271 | Sequence 271, App |
| | 7 | 24 | 100.0 | 619 | 18 | US-10-363-345A-4789 | Sequence 4789, Ap |
| c | 8 | 24 | 100.0 | 619 | 18 | US-10-363-345A-4790 | Sequence 4790, Ap |
| | 9 | 24 | 100.0 | 619 | 19 | US-10-363-483A-4789 | Sequence 4789, Ap |
| c | 10 | 24 | 100.0 | 619 | 19 | US-10-363-483A-4790 | Sequence 4790, Ap |
| | 11 | 24 | 100.0 | 734 | 18 | US-10-363-345A-19849 | Sequence 19849, A |
| c | 12 | 24 | 100.0 | 734 | 18 | US-10-363-345A-19850 | Sequence 19850, A |
| | 13 | 24 | 100.0 | 734 | 19 | US-10-363-483A-19849 | Sequence 19849, A |
| c | 14 | 24 | 100.0 | 734 | 19 | US-10-363-483A-19850 | Sequence 19850, A |
| | 15 | 24 | 100.0 | 6167 | 15 | US-10-240-453-244 | Sequence 244, App |
| | 16 | 23 | 95.8 | 23 | 17 | US-10-613-749-7 | Sequence 7, Appli |
| | 17 | 23 | 95.8 | 23 | 17 | US-10-613-749-12 | Sequence 12, Appl |
| | 18 | 23 | 95.8 | 1291 | 18 | US-10-363-345A-13853 | Sequence 13853, A |
| c | 19 | 23 | 95.8 | 1291 | 18 | US-10-363-345A-13854 | Sequence 13854, A |
| | 20 | 23 | 95.8 | 1291 | 19 | US-10-363-483A-13853 | Sequence 13853, A |
| c | 21 | 23 | 95.8 | 1291 | 19 | US-10-363-483A-13854 | Sequence 13854, A |
| | 22 | 22.4 | 93.3 | 24 | 17 | US-10-613-739-1 | Sequence 1, Appli |
| | 23 | 22.4 | 93.3 | 24 | 18 | US-10-816-220-150 | Sequence 150, App |
| | 24 | 22.4 | 93.3 | 24 | 18 | US-10-816-220-225 | Sequence 225, App |
| | 25 | 22.4 | 93.3 | 24 | 19 | US-10-644-052A-37 | Sequence 37, Appl |
| | 26 | 22.4 | 93.3 | 24 | 19 | US-10-644-052A-259 | Sequence 259, App |
| | 27 | 22.4 | 93.3 | 24 | 19 | US-10-644-052A-260 | Sequence 260, App |
| | 28 | 22.4 | 93.3 | 578 | 18 | US-10-363-345A-5395 | Sequence 5395, Ap |
| c | 29 | 22.4 | 93.3 | 578 | 18 | US-10-363-345A-5396 | Sequence 5396, Ap |
| | 30 | 22.4 | 93.3 | 578 | 19 | US-10-363-483A-5395 | Sequence 5395, Ap |
| c | 31 | 22.4 | 93.3 | 578 | 19 | US-10-363-483A-5396 | Sequence 5396, Ap |
| | 32 | 22.4 | 93.3 | 744 | 18 | US-10-363-345A-33711 | Sequence 33711, A |
| c | 33 | 22.4 | 93.3 | 744 | 18 | US-10-363-345A-33712 | Sequence 33712, A |
| | 34 | 22.4 | 93.3 | 744 | 19 | US-10-363-483A-33711 | Sequence 33711, A |
| c | 35 | 22.4 | 93.3 | 744 | 19 | US-10-363-483A-33712 | Sequence 33712, A |
| | 36 | 22 | 91.7 | 22 | 17 | US-10-613-749-8 | Sequence 8, Appli |
| | 37 | 22 | 91.7 | 22 | 17 | US-10-613-749-13 | Sequence 13, Appl |
| | 38 | 21.4 | 89.2 | 23 | 17 | US-10-613-739-67 | Sequence 67, Appl |
| | 39 | 21.4 | 89.2 | 23 | 17 | US-10-613-739-72 | Sequence 72, Appl |
| | 40 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-50 | Sequence 50, Appl |
| | 41 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-51 | Sequence 51, Appl |
| | 42 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-63 | Sequence 63, Appl |
| | 43 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-64 | Sequence 64, Appl |
| | 44 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-65 | Sequence 65, Appl |
| | 45 | 21.4 | 89.2 | 24 | 17 | US-10-613-739-66 | Sequence 66, Appl |

ALIGNMENTS

```
RESULT 1
US-10-613-749-1
; Sequence 1, Application US/10613749
; Publication No. US20040067905A1
; GENERAL INFORMATION:
;  APPLICANT: KRIEG, ARTHUR
;  TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS FOR STIMULATING IMMUNE RESPONSES
;  FILE REFERENCE: C01037.70041.US
;  CURRENT APPLICATION NUMBER: US/10/613,749
;  CURRENT FILING DATE:  2003-07-03
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Oligodeoxynucleotide
US-10-613-749-1

  Query Match             100.0%;  Score 24;  DB 17;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.88;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTCGTCGTTTCGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTCGTCGTTTCGTCGTT 24


RESULT 2
US-10-816-220-148
; Sequence 148, Application US/10816220
; Publication No. US20040235770A1
; GENERAL INFORMATION:
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GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 23:08:03 ; Search time 233 Seconds
(without alignments)
609.759 Million cell updates/sec

Title: US-10-613-749-1
Perfect score: 24
Sequence: 1 tcgtcgtttcgtcgtttcgtcgtt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 24 | 100.0 | 24 | 12 | ADI16070 | Adi16070 Immunosti |
| | 2 | 24 | 100.0 | 24 | 12 | ADK19224 | Adk19224 Immunosti |
| | 3 | 24 | 100.0 | 24 | 12 | ADK18989 | Adk18989 Immunosti |
| | 4 | 24 | 100.0 | 24 | 12 | ADK19223 | Adk19223 Immunosti |
| | 5 | 24 | 100.0 | 619 | 6 | ABQ18198 | Abq18198 Oligonucl |
| c | 6 | 24 | 100.0 | 619 | 6 | ABQ18199 | Abq18199 Oligonucl |
| c | 7 | 24 | 100.0 | 734 | 6 | ABQ33259 | Abq33259 Oligonucl |
| | 8 | 24 | 100.0 | 734 | 6 | ABQ33258 | Abq33258 Oligonucl |
| | 9 | 24 | 100.0 | 6167 | 6 | ABK28370 | Abk28370 DNA trans |
| | 10 | 23 | 95.8 | 23 | 12 | ADI16076 | Adi16076 Immunosti |
| | 11 | 23 | 95.8 | 23 | 12 | ADI16081 | Adi16081 Immunosti |
| | 12 | 23 | 95.8 | 1291 | 6 | ABQ27262 | Abq27262 Oligonucl |
| c | 13 | 23 | 95.8 | 1291 | 6 | ABQ27263 | Abq27263 Oligonucl |
| | 14 | 22.4 | 93.3 | 24 | 12 | ADI16114 | Adi16114 Immunosti |
| | 15 | 22.4 | 93.3 | 24 | 12 | ADK19213 | Adk19213 Immunosti |
| | 16 | 22.4 | 93.3 | 24 | 12 | ADK18990 | Adk18990 Immunosti |
| | 17 | 22.4 | 93.3 | 24 | 12 | ADK19212 | Adk19212 Immunosti |
| | 18 | 22.4 | 93.3 | 24 | 12 | ADO44306 | Ado44306 Nucleotid |
| c | 19 | 22.4 | 93.3 | 578 | 6 | ABQ18805 | Abq18805 Oligonucl |
| | 20 | 22.4 | 93.3 | 578 | 6 | ABQ18804 | Abq18804 Oligonucl |
| c | 21 | 22.4 | 93.3 | 744 | 6 | ABQ47121 | Abq47121 Oligonucl |
| | 22 | 22.4 | 93.3 | 744 | 6 | ABQ47120 | Abq47120 Oligonucl |
| | 23 | 22.4 | 93.3 | 10160 | 12 | ADP84798 | Adp84798 HIV subty |
| | 24 | 22.4 | 93.3 | 10186 | 12 | ADP84796 | Adp84796 Plasmid c |
| | 25 | 22.4 | 93.3 | 10198 | 12 | ADP84799 | Adp84799 HIV subty |
| | 26 | 22 | 91.7 | 22 | 12 | ADI16082 | Adi16082 Immunosti |
| | 27 | 22 | 91.7 | 22 | 12 | ADI16077 | Adi16077 Immunosti |
| | 28 | 21.4 | 89.2 | 23 | 12 | ADI16184 | Adi16184 Immunosti |
| | 29 | 21.4 | 89.2 | 23 | 12 | ADI16179 | Adi16179 Immunosti |
| | 30 | 21.4 | 89.2 | 24 | 12 | ADI16162 | Adi16162 Immunosti |
| | 31 | 21.4 | 89.2 | 24 | 12 | ADI16175 | Adi16175 Immunosti |
| | 32 | 21.4 | 89.2 | 24 | 12 | ADI16176 | Adi16176 Immunosti |
| | 33 | 21.4 | 89.2 | 24 | 12 | ADI16163 | Adi16163 Immunosti |
| | 34 | 21.4 | 89.2 | 24 | 12 | ADI16177 | Adi16177 Immunosti |
| | 35 | 21.4 | 89.2 | 24 | 12 | ADI16178 | Adi16178 Immunosti |
| | 36 | 21.4 | 89.2 | 24 | 12 | ADK19014 | Adk19014 Immunosti |
| | 37 | 21.4 | 89.2 | 24 | 12 | ADK19226 | Adk19226 Immunosti |
| | 38 | 21.4 | 89.2 | 24 | 12 | ADK19225 | Adk19225 Immunosti |
| | 39 | 21.4 | 89.2 | 24 | 12 | ADK19227 | Adk19227 Immunosti |
| | 40 | 21 | 87.5 | 21 | 12 | ADI16083 | Adi16083 Immunosti |
| | 41 | 21 | 87.5 | 21 | 12 | ADI16078 | Adi16078 Immunosti |
| | 42 | 21 | 87.5 | 701 | 6 | ABQ53878 | Abq53878 Oligonucl |
| c | 43 | 21 | 87.5 | 701 | 6 | ABQ53879 | Abq53879 Oligonucl |
| c | 44 | 21 | 87.5 | 716 | 6 | ABQ21055 | Abq21055 Oligonucl |
| | 45 | 21 | 87.5 | 716 | 6 | ABQ21054 | Abq21054 Oligonucl |

ALIGNMENTS

RESULT 1
ADI16070
ID ADI16070 standard; DNA; 24 BP.
XX
AC ADI16070;
XX
DT 22-APR-2004 (first entry)
XX
DE Immunostimulatory oligodeoxynucleotide ODN 10102 SEQ ID NO:1.
XX
KW ds; immunostimulatory; antibacterial; antiallergic; antiasthmatic;
KW cytostatic; virucide; fungicide; antiparasitic; interleukin antagonist;
KW gene therapy; infectious disease; allergy; asthma; cancer.
XX
OS Unidentified.
XX
PN WO2004005476-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US021113.
XX
PR 03-JUL-2002; 2002US-0393880P.
PR 03-JUL-2002; 2002US-0394090P.
PR 03-JUL-2002; 2002US-0394091P.
PR 03-JUL-2002; 2002US-0394164P.
PR 03-JUL-2002; 2002US-0394193P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Krieg AM;
XX
DR WPI; 2004-091353/09.
XX
PT New immunostimulatory nucleic acid molecule composition comprising CpG
PT motifs, useful for diagnosing, preventing and/or treating infectious
PT diseases, allergies, asthma and cancers.
XX
PS Claim 1; SEQ ID NO 1; 257pp; English.
XX
CC The invention relates to a novel composition comprising an
CC immunostimulatory nucleic acid molecule. A composition of the invention
CC has antibacterial, antiallergic, antiasthmatic, cytostatic, virucide,

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 00:48:18 ; Search time 1427 Seconds
(without alignments)
814.944 Million cell updates/sec

Title: US-10-613-749-1
Perfect score: 24
Sequence: 1 tcgtcgtttcgtcgtttcgtcgtt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in:*
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10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 6 | 20.8 | 86.7 | 24 | 6 | BD261142 | BD261142 Methods a |
| 7 | 20.8 | 86.7 | 24 | 6 | BD261298 | BD261298 Methods a |
| 8 | 20.8 | 86.7 | 24 | 6 | BD261563 | BD261563 Vaccine. |
| 9 | 20.8 | 86.7 | 24 | 6 | BD267904 | BD267904 Methods f |
| 10 | 20.8 | 86.7 | 24 | 6 | BD270804 | BD270804 Stereoiso |
| 11 | 20.8 | 86.7 | 24 | 6 | CQ769070 | CQ769070 Sequence |
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| 13 | 20.8 | 86.7 | 24 | 6 | CQ788202 | CQ788202 Sequence |
| 14 | 20.8 | 86.7 | 24 | 6 | CQ815138 | CQ815138 Sequence |
| 15 | 20.8 | 86.7 | 24 | 6 | CQ875565 | CQ875565 Sequence |
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ALIGNMENTS

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LOCUS AX323756 6167 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 244 from Patent WO0192565.
ACCESSION AX323756
VERSION AX323756.1 GI:18094504
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with dna transcription
JOURNAL Patent: WO 0192565-A 244 06-DEC-2001;
Epigenomics AG (DE)
FEATURES Location/Qualifiers
source 1. .6167
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 6167;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        760 TCGTCGTTTCGTCGTTTCGTCGTT 783
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WPCOMMENT
Sequence split into 32 fragments LOCUS BX571966 Accession BX571966

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| BX571966_01 | 100001 | 210000 |
| BX571966_02 | 200001 | 310000 |
| BX571966_03 | 300001 | 410000 |
| BX571966_04 | 400001 | 510000 |

GenCore version 5.1.6


OM nucleic - nucleic search, using sw model

Run on: April 7, 2005, 01:07:28 ; Search time 89 Seconds
(without alignments)
441.243 Million cell updates/sec

Title: US-10-613-749-1
Perfect score: 24
Sequence: 1 tcgtcgtttcgtcgtttcgtcgtt 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| | 2 | 20.8 | 86.7 | 24 | 3 | US-09-286-098-90 | Sequence 90, Appl |
| | 3 | 20.8 | 86.7 | 24 | 3 | US-08-960-774-46 | Sequence 46, Appl |
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| | 5 | 20.8 | 86.7 | 24 | 3 | US-09-082-649B-66 | Sequence 66, Appl |
| | 6 | 20.8 | 86.7 | 24 | 3 | US-09-325-193A-77 | Sequence 77, Appl |
| | 7 | 20.8 | 86.7 | 24 | 3 | US-09-191-170-84 | Sequence 84, Appl |
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| c | 20 | 17.6 | 73.3 | 894 | 4 | US-09-270-767-11695 | Sequence 11695, A |
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| c | 42 | 16.6 | 69.2 | 1499 | 2 | US-08-904-686A-3 | Sequence 3, Appli |
| c | 43 | 16.6 | 69.2 | 1499 | 3 | US-09-315-850-3 | Sequence 3, Appli |
| c | 44 | 16.6 | 69.2 | 6037 | 4 | US-09-902-540-800 | Sequence 800, App |
| c | 45 | 16.6 | 69.2 | 6039 | 1 | US-08-324-977-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-09-030-701-6
; Sequence 6, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-6

Query Match 86.7%; Score 20.8; DB 3; Length 24;
Best Local Similarity 91.7%; Pred. No. 2.3;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
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RESULT 2
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; Sequence 90, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105